

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/215,435

DATE: 01/06/1999
TIME: 18:52:04

Input Set: I215435.RAW

95 <212> TYPE: DNA
 96 <213> ORGANISM: Artificial Sequence
 97 <220> FEATURE:
 98 <223> OTHER INFORMATION: Oligonucleotide
 99 <400> SEQUENCE: 11
 100 atgggaaagg aaaagactca tatca 25
 101 <210> SEQ ID NO 12
 102 <211> LENGTH: 25
 103 <212> TYPE: DNA
 104 <213> ORGANISM: Artificial Sequence
 105 <220> FEATURE:
 106 <223> OTHER INFORMATION: Oligonucleotide
 107 <400> SEQUENCE: 12
 108 agcagcaaca atcaggacag cacag 25
 109 <210> SEQ ID NO 13
 110 <211> LENGTH: 25
 111 <212> TYPE: DNA
 112 <213> ORGANISM: Artificial Sequence
 113 <220> FEATURE:
 114 <223> OTHER INFORMATION: Oligonucleotide
 115 <400> SEQUENCE: 13
 116 atcaagaatt cgcacgagac catta 25
 117 <210> SEQ ID NO 14
 118 <211> LENGTH: 67
 119 <212> TYPE: DNA
 120 <213> ORGANISM: Artificial Sequence
 121 <220> FEATURE:
 122 <223> OTHER INFORMATION: Oligonucleotide
 123 <400> SEQUENCE: 14
 124 atcgttgaga ctcgtaccag cagagtcacg agagagacta cacggtactg gttttttttt 60
 W--> 125 tttttt *see item 10 on ERM summary sheet* 67
 126 <210> SEQ ID NO 15
 127 <211> LENGTH: 29
 128 <212> TYPE: DNA
 129 <213> ORGANISM: Artificial Sequence
 130 <220> FEATURE:
 131 <223> OTHER INFORMATION: Oligonucleotide
 132 <400> SEQUENCE: 15
 133 ccagcagagt cacgagagag actacacgg 29
 134 <210> SEQ ID NO 16
 135 <211> LENGTH: 25
 136 <212> TYPE: DNA
 137 <213> ORGANISM: Artificial Sequence
 138 <220> FEATURE:
 139 <223> OTHER INFORMATION: Oligonucleotide
 140 <400> SEQUENCE: 16
 141 cacgagagag actacacggt actgg 25
 142 <210> SEQ ID NO 17
 143 <211> LENGTH: 526
 144 <212> TYPE: DNA

PAGE: 4

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PATENT APPLICATION US/09/215,435DATE: 01/06/1999
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Input Set: I215435.RAW

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145 <213> ORGANISM: Homo sapiens
146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: complement(261..376)
149 <223> OTHER INFORMATION: blastn
150 <220> FEATURE:
151 <221> NAME/KEY: misc_feature
152 <222> LOCATION: complement(380..486)
153 <223> OTHER INFORMATION: blastn
154 <220> FEATURE:
155 <221> NAME/KEY: misc_feature
156 <222> LOCATION: complement(110..145)
157 <223> OTHER INFORMATION: blastn
158 <220> FEATURE:
159 <221> NAME/KEY: misc_feature
160 <222> LOCATION: complement(196..229)
161 <223> OTHER INFORMATION: blastn
162 <220> FEATURE:
163 <221> NAME/KEY: sig_peptide
164 <222> LOCATION: 90..140
165 <223> OTHER INFORMATION: Von Heijne matrix
166 <400> SEQUENCE: 17
167      aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca      60
168      gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc      113
169                               Met Lys Lys Val Leu Leu Leu Ile
170                               -15                               -10
171      aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag      161
172      Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
173                               -5                               1                               5
174      gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr      209
175      Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
176      10                               15                               20
177      wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att      257
178      Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
179      25                               30                               35
W--> 180      cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata      305
181      Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
182      40                               45                               50                               55
183      cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa      354
184      Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
185      60                               65
186      ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat      414
187      caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta      474
188      gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa      526
189 <210> SEQ ID NO 18
190 <211> LENGTH: 17
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
193 <220> FEATURE:
194 <221> NAME/KEY: SIGNAL

```

Please Note:

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields f each sequence which presents at least one n or Xaa.

*the previous
page and
this page
show as
samples
of error*

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/218,435

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
- 7 **Wrong Designation** Sequence(s) contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(1) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 **Use of N's or Xaa's (NEW RULES)** Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 **Use of <213>Organism (NEW RULES)** Sequence(s) are missing this mandatory field or its response.
- 12 **Use of <220>Feature (NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 **Wrong Format** File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.
AKS-Biotechnology Systems Branch- 7/10/98